

10/070778
STN Search Summary

=> d his

FILE 'CAPLUS' ENTERED AT 16:25:15 ON 03 MAY 2004

L1 83 S MURF
L2 5 S L1 AND (AERUGINOSA OR PSEUDOMONAS)

FILE 'REGISTRY' ENTERED AT 16:26:23 ON 03 MAY 2004

L3 0 S 6.3.2.10/RN
L4 0 S (6 3 2 10)/RN
L5 187 S MURF
L6 0 S (6 3 2 10) AND MURF
L7 1 S 6.3.2.10

FILE 'CAPLUS' ENTERED AT 16:27:59 ON 03 MAY 2004

L8 10 S L7
L9 10 S L8 NOT M5
L10 6 S L8 NOT L5
L11 0 S AERUGINOSA AND PEPTIDOGLYCIN
L12 131 S AERUGINOSA AND PEPTIDOGLYCAN
L13 24 S L12 AND (MUR?)
L14 22 S L13 NOT L2
L15 22 S L14 NOT L10

L2 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:536936 CAPLUS
TI In vitro reconstruction of the biosynthetic pathway of peptidoglycan
cytoplasmic precursor in Pseudomonas aeruginosa
AU El Zoeiby, A.; Sanschagrin, F.; Havugimana, P. C.; Garnier, A.; Levesque,
SO FEMS Microbiology Letters (2001), 201(2), 229-235

L2 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:232980 CAPLUS
TI The Cell Wall and Cell Division Gene Cluster in the Mra Operon of
Pseudomonas aeruginosa: Cloning, Production, and
Purification of Active Enzymes
AU Azzolina, Barbara A.; Yuan, Xiling; Anderson, Matt S.; El-Sherbeini,
Mohamed
SO Protein Expression and Purification (2001), 21(3), 393-400

L2 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:185769 CAPLUS
TI MurF gene encoding D-Alanyl-D-alanine-adding enzyme from
Pseudomonas aeruginosa and its use in antibiotic
screening

IN El-Sherbeini, Mohammed; Azzolina, Barbara

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2001018018	A1	20010315	WO 2000-US24437	20000906
PRAI US 1999-153293P	P	19990910		

L7 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2004 ACS on STN
RN 9023-60-3 REGISTRY
CN Synthetase, uridine diphosphoacetylmuramoylpentapeptide (9CI) (CA INDEX NAME)

OTHER NAMES:

CN E.C. 6.3.2.10
CN UDP-N-Acetylmuramoyl-L-alanyl-D-glutamyl-L-lysyl-D-alanyl-D-alanine synthetase
CN UDPacetylmuramoylpentapeptide synthetase
CN Uridine diphospho-N-acetylmuramoylalanyl-D-glutamyllysyl-D-alanyl-D-alanine synthetase
CN Uridine diphosphoacetylmuramoylpentapeptide synthetase

L10 ANSWER 2 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1989:150168 CAPLUS
TI Enzymes in the D-alanine branch of bacterial cell wall peptidoglycan assembly
AU Walsh, Christopher T.
SO Journal of Biological Chemistry (1989), 264(5), 2393-6
DT Journal; General **Review**

L10 ANSWER 5 OF 6 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1975:95132 CAPLUS
TI Formation of D-alanyl-D-alanine and D-alanine from UDPMurNAc-L-Ala-D-isoGlu-L-Lys-D-Ala-D-Ala by extracts of **Staphylococcus aureus** and **Streptococcus faecalis**
AU Oppenheim, B.; Patchornik, A.
SO FEBS Letters (1974), 48(2), 172-5

L15 ANSWER 2 OF 22 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2002:882942 CAPLUS
TI Bactericidal effect of gentamicin-induced **membrane vesicles derived from Pseudomonas aeruginosa** PA01 on gram-positive bacteria
AU MacDonald, Kelly L.; Beveridge, Terry J.
SO Canadian Journal of Microbiology (2002), 48(9), 810-820

L15 ANSWER 3 OF 22 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:918523 CAPLUS
TI Characterization of soluble and membrane-bound family 3 lytic transglycosylases from *Pseudomonas aeruginosa*
AU Blackburn, Neil T.; Clarke, Anthony J.
SO Biochemistry (2002), 41(3), 1001-1013

L15 ANSWER 4 OF 22 CAPLUS COPYRIGHT 2004 ACS on STN
AN 2001:33251 CAPLUS
TI Identification of Four Families of Peptidoglycan Lytic Transglycosylases
AU Blackburn, Neil T.; Clarke, Anthony J.
SO Journal of Molecular Evolution (2001), 52(1), 78-84

printed
L15 ANSWER 9 OF 22 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1998:681200 CAPLUS
TI Gram-negative bacteria produce membrane vesicles which are capable of killing other bacteria
AU Li, Zusheng; Clarke, Anthony J.; Beveridge, Terry J.
SO Journal of Bacteriology (1998), 180(20), 5478-5483

L15 ANSWER 11 OF 22 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1996:295774 CAPLUS
 TI Bacteriolytic effect of **membrane vesicles from Pseudomonas aeruginosa** on other bacteria including pathogens: conceptually new antibiotics
 AU Kadurugamuwa, Jagath L.; Beveridge, Terry J.
 SO Journal of Bacteriology (1996), 178(10), 2767-2774

L15 ANSWER 12 OF 22 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1996:278310 CAPLUS
 TI A major autolysin of **Pseudomonas aeruginosa**: subcellular distribution, potential role in cell growth and division, and secretion in surface membrane vesicles
 AU Li, Zusheng; Clarke, Anthony J.; Beveridge, Terry J.
 SO Journal of Bacteriology (1996), 178(9), 2479-2488

L15 ANSWER 16 OF 22 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1992:404105 CAPLUS
 TI Susceptibility of Pseudomonas species to the novel antibiotics mureidomycins
 AU Isono, Fujio; Kodama, Kentaro; Inukai, Masatoshi
 SO Antimicrobial Agents and Chemotherapy (1992), 36(5), 1024-7

L15 ANSWER 17 OF 22 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1991:160588 CAPLUS
 TI Mureidomycin A, a new inhibitor of bacterial peptidoglycan synthesis
 AU Isono, Fujio; Inukai, Masatoshi
 SO Antimicrobial Agents and Chemotherapy (1991), 35(2), 234-6

L15 ANSWER 19 OF 22 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1976:519199 CAPLUS
 TI Peptidoglycan of Pseudomonas aeruginosa
 AU Yanai, Akira; Kato, Keijiro; Beppu, Teruhiko; Arima, Kei
 SO Agricultural and Biological Chemistry (1976), 40(8), 1505-8

L15 ANSWER 21 OF 22 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1973:81922 CAPLUS
 TI Peptidoglycan of the cell walls of Pseudomonas aeruginosa
 AU Heilmann, Hans Dietrich
 SO European Journal of Biochemistry (1972), 31(3), 456-63

L15 ANSWER 22 OF 22 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 1971:10572 CAPLUS
 TI Cell walls of Pseudomonas species sensitive to ethylenediaminetetraacetic acid
 AU Wilkinson, Stephen G.
 SO Journal of Bacteriology (1970), 104(3), 1035-44

US-09-252-991A-7701
; Sequence 7701, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7701
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7701

Query Match 98.1%; Score 1421.8; DB 4; Length 1515;
Best Local Similarity 99.5%; Pred. No. 2.4e-269;
Matches 1426; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy	1	TCCGTTCTCCGACATCGAGCAGGCCGAGCGCGCCCTGGCCGCCTGGGAGGTGCCGCATGC	60
Db	83	TCCGTTCTCCGACATCGAGCAGGCCGAGCGCGCCCTGGCCGCCTGGGAGGTGCCGCATGC	142
Qy	61	TTGAGCCTCTTCGCCTCAGCCAGTTGACGGTCGCGCTGGACGCCCGCCTGATCGGCGAGG	120
Db	143	TTGAGCCTCTTCGCCTCAGCCAGTTGACGGTCGCGCTGGACGCCCGCCTGATCGGCGAGG	202
Qy	121	ACGCCGTCTTTTCGGCGGTTTCCACCGACAGTCGCGCCATCGGGCCCGGCCAACTGTTCA	180
Db	203	ACGCCGTCTTTTCGGCGGTTTCCACCGACAGTCGCGCCATCGGGCCCGGCCAACTGTTCA	262
Qy	181	TTGCCCTGAGTGGGCCGCGTTTCGACGGCCACGACTATCTCGCCGAGGTTGCCGCCAAGG	240
Db	263	TTGCCCTGAGTGGGCCGCGTTTCGACGGCCACGACTATCTCGCCGAGGTTGCCGCCAAGG	322
Qy	241	GCGCGGTGGCTGCGCTGGTGGAGCGCGAAGTCGCCGACGCGCCCTTGCCGCAATTGCTGG	300
Db	323	GCGCGGTGGCTGCGCTGGTGGAGCGCGAAGTCGCCGACGCGCCCTTGCCGCAATTGCTGG	382
Qy	301	TGCGCGATACCCGTGCGGCCCTGGGGCGACTGGGCGCGCTGAACCGGCGCAAGTTCACCG	360
Db	383	TGCGCGATACCCGTGCGGCCCTGGGGCGACTGGGCGCGCTGAACCGGCGCAAGTTCACCG	442
Qy	361	GCCCGCTGGCGGCCATGACGGGCTCCAGCGGCAAGACCGGGTCAAGGAGATGCTCGCCA	420
Db	443	GCCCGCTGGCGGCCATGACGGGCTCCAGCGGCAAGACCGGGTCAAGGAGATGCTCGCCA	502
Qy	421	GCATCCTGCGTACCCAGGCCGGCGATGCCGAGTCGGTGCTGGCTACCCGTGGCAATCTGA	480
Db	503	GCATCCTGTGTACCCAGGCCGGCGATGCCGAGTCGGTGCTGGCTACCCGTGGCAATCTGA	562

Qy	481	ACAACGACCTCGGCGTACCGCTGACCCTGCTGCAACTGGCGCCGAGCACCCTAGCGCAG	540
Db	563	ACAACGACCTCGGCGTACCGCTGACCCTGCTGCAACTGGCGCCGAGCACCCTAGCGCAG	622
Qy	541	TGATCGAACTGGGCGCCTCGCGCATCGGCGAGATCGCCTACACGGTCGAGCTGACCCGCC	600
Db	623	TGATCGAACTGGGCGCCTCGCGCATCGGCGAGATCGCCTACACGGTTGAGCTGACCCGCC	682
Qy	601	CGCACGTGGCGATCATCACCAATGCCGGAACCGCCCATGTCGGCGAGTTCGGCGGACCGG	660
Db	683	CGCACGTGGCGATCATCACCAATGCCGGAACCGCCCATGTCGGCGAGTTCGGCGGACCGG	742
Qy	661	AGAAGATCGTCGAGGCGAAGGGCGAGATACTCGAAGGGCTGGCCGCCGACGGCACCCGCC	720
Db	743	AGAAGATCGTCGAGGCGAAGGGCGAGATACTCGAAGGGCTGGCCGCCGACGGCACCCGCC	802
Qy	721	TACTGAACCTGGACGACAAGGCCTTCGACACCTGGAAGGCCCGTGCCAGCGGCCGTCCGT	780
Db	803	TGCTGAACCTGGACGACAAGGCCTTCGACACCTGGAAGGCCCGTGCCAGCGGCCGTCCGT	862
Qy	781	TGCTGACTTTCTCCCTCGACCGGCCCCAGGCCGATTTCCGCGCCGCCGATCTGCAGCGCG	840
Db	863	TGCTGACTTTCTCCCTCGACCGGCCCCAGGCCGATTTCCGCGCCGCCGATCTGCAGCGCG	922
Qy	841	ATGCGCGCGGCTGCATGGGCTTCAGGCTGCAGGGCGTAGCGGGTGAAGCGCAGGTCCAGC	900
Db	923	ATGCGCGTGCTGCATGGGCTTCAGGCTGCAGGGCGTAGCGGGTGAAGCGCAGGTCCAGC	982
Qy	901	TCAACCTGCTGGGGCGGCACAATGTCGCCAATGCCCTGGCTGCGGCCGCTGCCGCCCATG	960
Db	983	TCAACCTGCTGGGGCGGCACAATGTCGCCAATGCCCTGGCTGCGGCCGCTGCCGCCCATG	1042
Qy	961	CACTGGGCGTGCCGCTGGATGGGATCGTCGCCGGGCTGCAGGCGCTGCAGCCGGTCAAGG	1020
Db	1043	CACTGGGCGTGCCGCTGGATGGGATCGTCGCCGGGCTGCAGGCGCTGCAGCCGGTCAAGG	1102
Qy	1021	GCCGCGCGGTAGCGCAACTGACCGCCAGCGGGCTGCGTGTGATAGACGACAGCTACAACG	1080
Db	1103	GCCGCGCGGTAGCGCAACTGACCGCCAGCGGGCTGCGTGTGATAGACGACAGCTACAACG	1162
Qy	1081	CCAACCCCGCGTCAATGCTGGCGGCGATTGATATACTGAGCGGCTTTTCCGGGCGCACCG	1140
Db	1163	CCAACCCCGCGTCAATGCTGGCGGCGATTGATATACTGAGCGGCTTTTCCGGGCGCACCG	1222
Qy	1141	TCCTGGTCCTCGGAGACATGGGCGAACTCGGTTCTGGGCCGAGCAGGCCACCGCGAGG	1200
Db	1223	TCCTGGTCCTCGGAGACATGGGCGAACTCGGTTCTGGGCCGAGCAGGCCACCGCGAGG	1282
Qy	1201	TGGGCGCCTACGCCGCTGGCAAGGTGTCCGCGCTCTATGCGGTCGGACCGCTGATGGCCC	1260
Db	1283	TGGGCGCCTACGCCGCTGGCAAGGTGTCCGCGCTCTATGCGGTCGGACCGCTGATGGCCC	1342
Qy	1261	ACGCCGTACAGGCGTTCGGCGCCACGGGCCGGCACTTCGCCGACCAGGCCAGCCTGATCG	1320
Db	1343	ACGCCGTACAGGCGTTCGGCGCCACGGGCCGGCACTTCGCCGACCAGGCCAGCCTGATCG	1402

Qy	1321	GGGCGCTGGCCACCGAACAACCGACAACCACCATT	TTTGATCAAGGGT	CCCCGCAGTGC	CGG	1380
Db	1403	GGGCGCTGGCCACCGAACAACCGACAACCACCATT	TTTGATCAAGGGT	CCCCGCAGTGC	CGG	1462
Qy	1381	CGATGGACAAAGTCGTCGCGGCGCTGTGCGGTT	CCTCCGAGGAGAGTCACTAA			1433
Db	1463	CGATGGACAAAGTCGTCGCGGCGCTGTGCGGTT	CCTCCGAGGAGAGTCACTAA			1515

US-09-252-991A-7701

Alignment Scores:

Pred. No.:	6.52e-224	Length:	1515
Score:	2250.00	Matches:	456
Percent Similarity:	99.56%	Conservative:	0
Best Local Similarity:	99.56%	Mismatches:	2
Query Match:	99.47%	Indels:	0
DB:	4	Gaps:	0

US-10-070-778-2 (1-458) x US-09-252-991A-7701 (1-1515)

Qy	1	MetLeuGluProLeuArgLeuSerGlnLeuThrValAlaLeuAspAlaArgLeuIleGly	20
Db	139	ATGCTTGAGCCTCTTCGCCTCAGCCAGTTGACGGTCGCGCTGGACGCCCGCCTGATCGGC	198
Qy	21	GluAspAlaValPheSerAlaValSerThrAspSerArgAlaIleGlyProGlyGlnLeu	40
Db	199	GAGGACGCCGTCTTTTCGGCGGTTTCCACCGACAGTCGCGCCATCGGGCCCGGCCAACTG	258
Qy	41	PheIleAlaLeuSerGlyProArgPheAspGlyHisAspTyrLeuAlaGluValAlaAla	60
Db	259	TTCATTGCCCTGAGTGGGCCGCGTTTCGACGGCCACGACTATCTCGCCGAGGTTGCCGCC	318
Qy	61	LysGlyAlaValAlaAlaLeuValGluArgGluValAlaAspAlaProLeuProGlnLeu	80
Db	319	AAGGGCGCGGTGGCTGCGCTGGTGGAGCGCGAAGTCGCCGACGCGCCCCTGCCGCAATTG	378
Qy	81	LeuValArgAspThrArgAlaAlaLeuGlyArgLeuGlyAlaLeuAsnArgArgLysPhe	100
Db	379	CTGGTGCGCGATACCCGTGCGGCCCTGGGGCGACTGGGCGCGCTGAACCGGCGCAAGTTC	438
Qy	101	ThrGlyProLeuAlaAlaMetThrGlySerSerGlyLysThrAlaValLysGluMetLeu	120
Db	439	ACCGGCCCGCTGGCGGCCATGACGGGCTCCAGCGGCAAGACCACGGTCAAGGAGATGCTC	498
Qy	121	AlaSerIleLeuArgThrGlnAlaGlyAspAlaGluSerValLeuAlaThrArgGlyAsn	140
Db	499	GCCAGCATCCTGTGTACCCAGGCCGGCGATGCCGAGTCGGTGCTGGCTACCCGTGGCAAT	558
Qy	141	LeuAsnAsnAspLeuGlyValProLeuThrLeuLeuGlnLeuAlaProGlnHisArgSer	160
Db	559	CTGAACAACGACCTCGGCGTACCGCTGACCCTGCTGCAACTGGCGCCGCAGCACCGTAGC	618
Qy	161	AlaValIleGluLeuGlyAlaSerArgIleGlyGluIleAlaTyrThrValGluLeuThr	180
Db	619	GCAGTGATCGAACTGGGCGCCTCGCGCATCGGCGAGATCGCCTACACGGTTGAGCTGACC	678
Qy	181	ArgProHisValAlaIleIleThrAsnAlaGlyThrAlaHisValGlyGluPheGlyGly	200
Db	679	CGCCCGCACGTGGCGATCATCACC AATGCCGGAACCGCCCATGTCGGCGAGTTGGCGGA	738
Qy	201	ProGluLysIleValGluAlaLysGlyGluIleLeuGluGlyLeuAlaAlaAspGlyThr	220
Db	739	CCGGAGAAGATCGTCGAGGCGAAGGGCGAGATACTCGAAGGGCTGGCCGCCGACGGCACC	798

Qy	221	AlaValLeuAsnLeuAspAspLysAlaPheAspThrTrpLysAlaArgAlaSerGlyArg	240
Db	799	GCCGTGCTGAACCTGGACGACAAGGCCTTCGACACCTGGAAGGCCCGTGCCAGCGGCCGT	858
Qy	241	ProLeuLeuThrPheSerLeuAspArgProGlnAlaAspPheArgAlaAlaAspLeuGln	260
Db	859	CCGTTGCTGACTTTCTCCCTCGACCGGCCCCAGGCCGATTTCCGCGCCGCCGATCTGCAG	918
Qy	261	ArgAspAlaArgGlyCysMetGlyPheArgLeuGlnGlyValAlaGlyGluAlaGlnVal	280
Db	919	CGCGATGCGCGTGGCTGCATGGGCTTCAGGCTGCAGGGCGTAGCGGGTGAAGCGCAGGTC	978
Qy	281	GlnLeuAsnLeuLeuGlyArgHisAsnValAlaAsnAlaLeuAlaAlaAlaAlaAla	300
Db	979	CAGCTCAACCTGCTGGGGCGGCACAATGTCGCAATGCCCTGGCTGCCGCCGCTGCCGCC	1038
Qy	301	HisAlaLeuGlyValProLeuAspGlyIleValAlaGlyLeuGlnAlaLeuGlnProVal	320
Db	1039	CATGCACTGGGCGTGCCGCTGGATGGGATCGTCGCCGGGCTGCAGGCGCTGCAGCCGGTC	1098
Qy	321	LysGlyArgAlaValAlaGlnLeuThrAlaSerGlyLeuArgValIleAspAspSerTyr	340
Db	1099	AAGGGCCGCGCGGTAGCGCAACTGACGCCAGCGGGCTGCGTGTGATAGACGACAGCTAC	1158
Qy	341	AsnAlaAsnProAlaSerMetLeuAlaAlaIleAspIleLeuSerGlyPheSerGlyArg	360
Db	1159	AACGCCAACCCGCGTCAATGCTGGCGGCGATTGATATACTGAGCGGCTTTTCCGGGCGC	1218
Qy	361	ThrValLeuValLeuGlyAspMetGlyGluLeuGlySerTrpAlaGluGlnAlaHisArg	380
Db	1219	ACCGTCCTGGTCCTCGGAGACATGGGCGAACTCGGTTCTTGGGCCGAGCAGGCCACCGC	1278
Qy	381	GluValGlyAlaTyrAlaAlaGlyLysValSerAlaLeuTyrAlaValGlyProLeuMet	400
Db	1279	GAGGTGGGCGCCTACGCCGCTGGCAAGGTGTCCGCGCTCTATGCGGTGCGACCGCTGATG	1338
Qy	401	AlaHisAlaValGlnAlaPheGlyAlaThrGlyArgHisPheAlaAspGlnAlaSerLeu	420
Db	1339	GCCACGCCGTACAGGCGTTGGGCGCCACGGCCGGCACTTCGCCGACCAGGCCAGCCTG	1398
Qy	421	IleGlyAlaLeuAlaThrGluGlnProThrThrThrIleLeuIleLysGlySerArgSer	440
Db	1399	ATCGGGGCGCTGGCCACCGAACAACCGACAACCACCATTTTGATCAAGGGTTCCCGCAGT	1458
Qy	441	AlaAlaMetAspLysValValAlaAlaLeuCysGlySerSerGluGluSerHis	458
Db	1459	GCGGCGATGGACAAAGTCGTCGCGCGCTGTGCGGTTCTCCGAGGAGAGTCAC	1512

Sequence Search Summary

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2004, 01:45:30 ; Search time 594 Seconds
(without alignments)
10363.029 Million cell updates/sec

Title: US-10-070-778-1
Perfect score: 1449
Sequence: 1 tccgttctccgacatcgagc.....ctaatgctcctgctgctggc 1449.

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

SEQ ID NO: 1+2
in DNA databases

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1449	100.0	1449	4	AAS01762	Aas01762 Pseudomon
2	1372.2	94.7	1377	4	AAS54277	Aas54277 Pseudomon
3	1372.2	94.7	1377	7	ACA42600	Aca42600 Prokaryot
4	695.6	48.0	1365	7	ACA44261	Aca44261 Prokaryot
5	692.4	47.8	1356	7	ACA45660	Aca45660 Prokaryot
6	317	21.9	2835	7	ACA27387	Aca27387 Prokaryot
7	296	20.4	1404	7	ACA26293	Aca26293 Prokaryot

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2004, 03:40:40 ; Search time 133 Seconds
(without alignments)
6046.044 Million cell updates/sec

Title: US-10-070-778-1
Perfect score: 1449
Sequence: 1 tccgttctccgacatcgagc.....ctaatgctcctgctgctggc 1449

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
c	1	1421.8	98.1	1515	4	US-09-252-991A-7701			Sequence 7701, Ap
	2	1079.8	74.5	1215	4	US-09-252-991A-7862			Sequence 7862, Ap
	3	338	23.3	1404	4	US-09-252-991A-7623			Sequence 7623, Ap
	4	288.8	19.9	1437	4	US-09-489-039A-5205			Sequence 5205, Ap
c	5	268.6	18.5	1360	2	US-08-732-612-1			Sequence 1, Appli
	6	214	14.8	1611	4	US-09-252-991A-7930			Sequence 7930, Ap
c	7	139.8	9.6	4411529	3	US-09-103-840A-1			Sequence 1, Appli
c	8	137.2	9.5	4403765	3	US-09-103-840A-2			Sequence 2, Appli
	9	134	9.2	1419	4	US-09-543-681A-2913			Sequence 2913, Ap
	10	123.8	8.5	1830121	4	US-09-557-884-1			Sequence 1, Appli
	11	123.8	8.5	1830121	4	US-09-643-990A-1			Sequence 1, Appli

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 24, 2004, 05:32:38 ; Search time 528 Seconds
(without alignments)
10151.654 Million cell updates/sec

Title: US-10-070-778-1
Perfect score: 1449
Sequence: 1 tccgttctccgacatcgagc.....ctaagtctcctgctgctggc 1449

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description	
	No.	Score	Query Match Length	DB	ID		
	1	1372.2	94.7	1377	9	US-09-815-242-7914	Sequence 7914, Ap
	2	1372.2	94.7	1377	12	US-10-282-122A-30470	Sequence 30470, A
	3	695.6	48.0	1365	12	US-10-282-122A-32131	Sequence 32131, A
	4	692.4	47.8	1356	12	US-10-282-122A-33530	Sequence 33530, A
	5	317	21.9	2835	12	US-10-282-122A-15257	Sequence 15257, A
	6	296	20.4	1404	12	US-10-282-122A-14163	Sequence 14163, A
	7	290.6	20.1	1356	12	US-10-282-122A-23403	Sequence 23403, A
	8	278	19.2	1359	9	US-09-741-669-257	Sequence 257, App
	9	278	19.2	1359	9	US-09-815-242-5930	Sequence 5930, Ap
	10	278	19.2	1359	12	US-10-282-122A-20227	Sequence 20227, A
	11	252	17.4	1356	12	US-10-282-122A-19658	Sequence 19658, A
	12	247.2	17.1	1359	12	US-10-282-122A-39833	Sequence 39833, A
	13	246.2	17.0	1359	9	US-09-815-242-9976	Sequence 9976, Ap
	14	244.2	16.9	1410	12	US-10-282-122A-12920	Sequence 12920, A
	15	244	16.8	1359	12	US-10-282-122A-38999	Sequence 38999, A
	16	218	15.0	1362	12	US-10-282-122A-41276	Sequence 41276, A
	17	217.6	15.0	1158	12	US-10-282-122A-11387	Sequence 11387, A
	18	204.4	14.1	1364	12	US-10-282-122A-37048	Sequence 37048, A
	19	194.6	13.4	1377	12	US-10-282-122A-41735	Sequence 41735, A
	20	192	13.3	1413	14	US-10-156-761-6095	Sequence 6095, Ap
	21	192	13.3	9025608	14	US-10-156-761-1	Sequence 1, Appli
	22	187.4	12.9	1308	12	US-10-282-122A-28948	Sequence 28948, A
	23	184.2	12.7	1359	12	US-10-282-122A-29881	Sequence 29881, A
	24	139.8	9.6	1533	9	US-09-712-363-81	Sequence 81, Appl
	25	139.8	9.6	1533	12	US-10-282-122A-28471	Sequence 28471, A
c	26	138.8	9.6	1647	12	US-10-282-122A-28781	Sequence 28781, A
	27	129.4	8.9	1380	12	US-10-282-122A-32631	Sequence 32631, A
	28	126	8.7	1383	12	US-10-282-122A-30711	Sequence 30711, A
	29	123.8	8.5	1374	9	US-09-815-242-7088	Sequence 7088, Ap
	30	123.8	8.5	1374	12	US-10-282-122A-22234	Sequence 22234, A
	31	123.8	8.5	1830121	14	US-10-329-960-1	Sequence 1, Appli
	32	123.8	8.5	1830121	15	US-10-329-670-1	Sequence 1, Appli
	33	94.6	6.5	1482	12	US-10-282-122A-26873	Sequence 26873, A
	34	85.6	5.9	1488	12	US-10-282-122A-17843	Sequence 17843, A
	35	82.6	5.7	1398	12	US-10-282-122A-8531	Sequence 8531, Ap
	36	81.8	5.6	981	12	US-10-282-122A-25880	Sequence 25880, A
	37	77.2	5.3	1518	14	US-10-156-761-6094	Sequence 6094, Ap
	38	73.4	5.1	1542	9	US-09-738-626-2369	Sequence 2369, Ap
c	39	73.4	5.1	3309400	9	US-09-738-626-1	Sequence 1, Appli
	40	69.4	4.8	15738	14	US-10-329-079-12	Sequence 12, Appl
	41	69.4	4.8	37360	14	US-10-329-079-6	Sequence 6, Appli
	42	69.2	4.8	894	12	US-10-282-122A-11787	Sequence 11787, A
	43	68	4.7	708	12	US-10-282-122A-12357	Sequence 12357, A
	44	67.6	4.7	822	14	US-10-156-761-3410	Sequence 3410, Ap
c	45	66.4	4.6	77536	10	US-09-940-316B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-815-242-7914

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OM nucleic - nucleic search, using sw model

Run on: March 24, 2004, 03:38:31 ; Search time 3537 Seconds
(without alignments)
12233.616 Million cell updates/sec

Title: US-10-070-778-1
Perfect score: 1449
Sequence: 1 tccgttctccgacatcgagc.....ctaattgctcctgctgctggc 1449

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result	Query						
No.	Score	Match	Length	DB	ID	Description	
	1	610.2	42.1	1108	28	BZ559252	BZ559252 pacs2-164
c	2	566.8	39.1	1214	28	BZ572325	BZ572325 msh2_2585
	3	441.8	30.5	1215	28	BZ575690	BZ575690 msh2_4579
c	4	416	28.7	666	28	BZ572149	BZ572149 msh2_2530
	5	407.8	28.1	1026	28	BZ559351	BZ559351 pacs2-164
c	6	149.8	10.3	838	28	CC115454	CC115454 NDL.42F3.
c	7	145.2	10.0	685	28	CC140248	CC140248 NDL.42F4.
c	8	127.6	8.8	684	28	AQ968325	AQ968325 LERJB56TR
	9	127.2	8.8	817	29	CNS01IUM	AL146223 Anopheles
c	10	125.8	8.7	346	10	BF837914	BF837914 RC0-HT095
	11	88.2	6.1	1285	28	BZ575700	BZ575700 msh2_4583
c	12	80.6	5.6	508	9	AV629852	AV629852 AV629852
c	13	74.6	5.1	925	29	CNS0091P	AL053013 Drosophil
	14	68.8	4.7	925	29	CNS0091P	AL053013 Drosophil
	15	68.8	4.7	1610	28	BZ569386	BZ569386 pacs2-164
	16	67.4	4.7	982	13	BX415111	BX415111 BX415111
	17	67.2	4.6	1189	29	AG030608	AG030608 Pan trogl
	18	67.2	4.6	1201	13	BX405071	BX405071 BX405071
	19	64.2	4.4	1798	29	AG171124	AG171124 Pan trogl
	20	63.6	4.4	893	28	AZ193531	AZ193531 SP_1023_B
c	21	63.6	4.4	1610	28	BZ569386	BZ569386 pacs2-164
c	22	63.4	4.4	911	29	CC704337	CC704337 OGUGX11TV
	23	63.4	4.4	915	29	CG352123	CG352123 OGXBA55TV
c	24	63.2	4.4	1189	29	AG030608	AG030608 Pan trogl
	25	63	4.3	998	29	AG046208	AG046208 Pan trogl
c	26	62	4.3	1421	28	BZ569488	BZ569488 pacs2-164
c	27	61.8	4.3	1134	29	AG061098	AG061098 Pan trogl
	28	60.8	4.2	494	12	BG455820	BG455820 NF070E07P
c	29	60.6	4.2	1015	28	BZ569259	BZ569259 pacs2-164
	30	60.4	4.2	564	29	CG224720	CG224720 OG2AT66TV
c	31	60.4	4.2	663	29	CG245199	CG245199 OG0DZ87TH
	32	60.4	4.2	1542	29	AG032943	AG032943 Pan trogl
c	33	59.6	4.1	911	29	AG043617	AG043617 Pan trogl
	34	59.2	4.1	1145	29	AG082667	AG082667 Pan trogl
	35	59	4.1	706	14	CF243689	CF243689 3530_1_23
	36	59	4.1	849	29	CG343694	CG343694 OGWIQ64TV
c	37	58.8	4.1	1637	28	BZ572329	BZ572329 msh2_2586
c	38	58.6	4.0	807	29	CG271592	CG271592 OG3CW52TH
	39	58.6	4.0	831	29	CC722906	CC722906 OGKAU13TH
	40	58.6	4.0	835	14	CB904973	CB904973 tric040xn
	41	58.6	4.0	835	14	CF876206	CF876206 tric040xn
	42	58.6	4.0	935	29	CG271603	CG271603 OG3CW52TV
c	43	58.6	4.0	1093	13	BQ939664	BQ939664 AGENCOURT
c	44	58.4	4.0	1956	29	CG754548	CG754548 P050-1-A1
	45	58.2	4.0	562	29	CG055749	CG055749 PUICM11TB

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OM nucleic - nucleic search, using sw model

Run on: March 24, 2004, 02:36:25 ; Search time 5617 Seconds
(without alignments)
11181.068 Million cell updates/sec

Title: US-10-070-778-1
Perfect score: 1449
Sequence: 1 tccgttctccgacatcgagc.....ctaatgctcctgctgctggc 1449

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	1449	100.0	5280	1	AY008276		AY008276	Pseudomon
c	2	1444.2	99.7	24000	1	AE004856		AE004856	Pseudomon
	3	734	50.7	301995	1	AE016779		AE016779	Pseudomon
c	4	732	50.5	311600	1	AE016871		AE016871	Pseudomon
c	5	390.2	26.9	208524	1	AE016925		AE016925	Chromobac
c	6	323.4	22.3	344805	1	BX640434		BX640434	Bordetell
c	7	320.2	22.1	348074	1	BX640449		BX640449	Bordetell
c	8	317	21.9	348134	1	BX640420		BX640420	Bordetell
	9	308.6	21.3	13045	1	AE012171		AE012171	Xanthomon
c	10	296.8	20.5	188050	1	AL646072		AL646072	Ralstonia
	11	288.8	19.9	1437	6	AR388476		AR388476	Sequence
	12	281.2	19.4	11441	1	AE015046		AE015046	Shigella
	13	281.2	19.4	290029	1	AE016978		AE016978	Shigella
	14	279.6	19.3	1800	1	ECU67891		ECU67891	Escherichia
	15	278	19.2	1359	6	AX189056		AX189056	Sequence
	16	278	19.2	1800	1	ECU67893		ECU67893	Escherichia
	17	278	19.2	12791	1	AE005185		AE005185	Escherich
	18	278	19.2	21757	1	AE000118		AE000118	Escherich
	19	278	19.2	281530	1	AP002550		AP002550	Escherich
	20	276.4	19.1	1491	1	ECMURF		X15432	E. coli mur
	21	276.4	19.1	28277	6	AX191720		AX191720	Sequence
	22	276.4	19.1	28277	15	EC2MIN		X55034	E. coli 2 m
	23	276.4	19.1	111408	1	ECO110K		D10483	Escherichia
	24	275.6	19.0	13079	1	AE011708		AE011708	Xanthomon
c	25	275.6	19.0	212737	2	AC147207		AC147207	Silurana
	26	266.8	18.4	300409	1	AE016755		AE016755	Escherich
	27	247.2	17.1	251050	1	AL627265		AL627265	Salmonell
	28	247.2	17.1	300169	1	AE016834		AE016834	Salmonell
	29	244	16.8	22348	1	AE008699		AE008699	Salmonell
c	30	218	15.0	22201	1	AE004310		AE004310	Vibrio ch
c	31	214.8	14.8	69301	1	STU82965		U82965	Streptomcye
	32	213.4	14.7	301727	1	AE016960		AE016960	Coxiella
	33	213.4	14.7	316050	1	BX321859		BX321859	Nitrosomo

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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 24, 2004, 06:34:44 ; Search time 2793 Seconds
(without alignments)
4896.842 Million cell updates/sec

Title: US-10-070-778-2
Perfect score: 2262
Sequence: 1 MLEPLRLSQLTVALDARLIG.....RSAAMDKVVAALCGSSEESH 458

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10070778/runat_23032004_141617_6672/app_query.fasta_1.
647

-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10070778 @CGN_1_1_4237 @runat_23032004_141617_6672 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*

11: gb_htc:*
 12: gb_est3:*
 13: gb_est4:*
 14: gb_est5:*
 15: em_estfun:*
 16: em_estom:*
 17: em_gss_hum:*
 18: em_gss_inv:*
 19: em_gss_pln:*
 20: em_gss_vrt:*
 21: em_gss_fun:*
 22: em_gss_mam:*
 23: em_gss_mus:*
 24: em_gss_pro:*
 25: em_gss_rod:*
 26: em_gss_phg:*
 27: em_gss_vrl:*
 28: gb_gss1:*
 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	1074	47.5	1108	28	BZ559252			BZ559252 pacs2-164
c	2	950.5	42.0	1214	28	BZ572325			BZ572325 msh2_2585
	3	779.5	34.5	1215	28	BZ575690			BZ575690 msh2_4579
c	4	691.5	30.6	666	28	BZ572149			BZ572149 msh2_2530
	5	646	28.6	1026	28	BZ559351			BZ559351 pacs2-164
c	6	434	19.2	838	28	CC115454			CC115454 NDL.42F3.
c	7	423.5	18.7	684	28	AQ968325			AQ968325 LERJB56TR
c	8	403	17.8	685	28	CC140248			CC140248 NDL.42F4.
	9	384	17.0	817	29	CNS01IUM			AL146223 Anopheles
	10	279.5	12.4	623	14	CB095990			CB095990 ie98f06.b
c	11	273.5	12.1	346	10	BF837914			BF837914 RC0-HT095
c	12	210	9.3	6303	28	BH771012			BH771012 LIMGtag73
	13	208.5	9.2	494	12	BG455820			BG455820 NF070E07P
	14	185	8.2	740	12	BI727187			BI727187 1031090D0
c	15	184.5	8.2	1445	28	BZ568959			BZ568959 pacs2-164
	16	168.5	7.4	646	12	BM000662			BM000662 1031090D0
	17	160.5	7.1	437	28	AZ303140			AZ303140 GSSBru208
c	18	149.5	6.6	1289	29	CG746186			CG746186 P039-2-D0
	19	148	6.5	786	28	BH541774			BH541774 BOGWV43TF
c	20	146	6.5	1100	14	CK214645			CK214645 FGAS02657
	21	145	6.4	597	10	AW200691			AW200691 se92c10.y
c	22	144	6.4	987	28	BZ568302			BZ568302 pacs2-164
	23	141.5	6.3	3721	11	BC032414			BC032414 Homo sapi
	24	138.5	6.1	481	28	AZ048545			AZ048545 GSSBru067
c	25	134	5.9	508	9	AV629852			AV629852 AV629852
	26	133.5	5.9	564	14	CA938683			CA938683 sav36d04.
c	27	133.5	5.9	697	14	CF887565			CF887565 UI-CF-FN0
	28	133.5	5.9	739	13	BQ852657			BQ852657 QGB18J24.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 24, 2004, 07:49:39 ; Search time 4484 Seconds
(without alignments)
4427.098 Million cell updates/sec

Title: US-10-070-778-2
Perfect score: 2262
Sequence: 1 MLEPLRLSQLTVALDARLIG.....RSAAMDKVVAALCGSSEESH 458

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10070778/runat_23032004_141616_6662/app_query.fasta_1.
647

-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10070778_@CGN_1_1_5265_@runat_23032004_141616_6662 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*

```

11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%					Description
	No.	Score	Match	Length	ID	
	1	2262	100.0	5280	1 AY008276	AY008276 Pseudomon
c	2	2258	99.8	24000	1 AE004856	AE004856 Pseudomon
c	3	1631	72.1	311600	1 AE016871	AE016871 Pseudomon
	4	1603.5	70.9	301995	1 AE016779	AE016779 Pseudomon
	5	962	42.5	301727	1 AE016960	AE016960 Coxiella
	6	921.5	40.7	11441	1 AE015046	AE015046 Shigella
	7	921.5	40.7	290029	1 AE016978	AE016978 Shigella
	8	917.5	40.6	1359	6 AX189056	AX189056 Sequence
	9	917.5	40.6	1800	1 ECU67891	U67891 Escherichia
	10	917.5	40.6	21757	1 AE000118	AE000118 Escherich
	11	913.5	40.4	1800	1 ECU67893	U67893 Escherichia
	12	911.5	40.3	12791	1 AE005185	AE005185 Escherich
	13	911.5	40.3	281530	1 AP002550	AP002550 Escherich
	14	910.5	40.3	1491	1 ECMURF	X15432 E. coli mur
	15	910.5	40.3	28277	6 AX191720	AX191720 Sequence
	16	910.5	40.3	28277	15 EC2MIN	X55034 E. coli 2 m

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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 24, 2004, 06:31:50 ; Search time 488 Seconds
(without alignments)
3987.038 Million cell updates/sec

Title: US-10-070-778-2
Perfect score: 2262
Sequence: 1 MLEPLRLSQLTVALDARLIG.....RSAAMDKVVAALCGSSEESH 458

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10070778/runat_23032004_141616_6654/app_query.fasta_1.
647

-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10070778 @CGN_1_1_708 @runat_23032004_141616_6654 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query					
No.	Score	Match	Length	DB	ID		Description	
1	2262	100.0	1449	4	AAS01762		Aas01762	Pseudomon
2	2258	99.8	1377	4	AAS54277		Aas54277	Pseudomon
3	2258	99.8	1377	7	ACA42600		Aca42600	Prokaryot
4	1616	71.4	1356	7	ACA45660		Aca45660	Prokaryot
5	1603.5	70.9	1365	7	ACA44261		Aca44261	Prokaryot
6	917.5	40.6	1359	4	AAS52293		Aas52293	E. coli D
7	917.5	40.6	1359	5	AAH81458		Aah81458	Escherich
8	917.5	40.6	1359	7	ACA32357		Aca32357	Prokaryot
9	885.5	39.1	1360	2	AAT63360		Aat63360	Temperatu
10	885.5	39.1	1360	2	AAX86095		Aax86095	Nucleotid
11	882.5	39.0	1356	7	ACA31788		Aca31788	Prokaryot
12	880.5	38.9	1359	7	ACA51129		Aca51129	Prokaryot
13	879.5	38.9	1356	7	ACA35533		Aca35533	Prokaryot
14	875.5	38.7	1362	7	ACA53406		Aca53406	Prokaryot
15	874	38.6	1404	7	ACA26293		Aca26293	Prokaryot
16	872.5	38.6	1380	7	ACF71680		Acf71680	Photorhab
17	872.5	38.6	110000	7	ACF67367_48		Continuation (49 o	
18	872.5	38.6	110000	7	ACF65387_0		Acf65387	Photorhab
19	871.5	38.5	1359	7	ACA51963		Aca51963	Prokaryot
20	870.5	38.5	1359	4	AAS56339		Aas56339	Salmonell
21	857	37.9	1377	7	ACA53865		Aca53865	Prokaryot
22	828	36.6	1410	7	ACA25050		Aca25050	Prokaryot
23	819	36.2	1380	7	ACA44761		Aca44761	Prokaryot
24	812	35.9	1374	4	AAS53451		Aas53451	Haemophil
25	812	35.9	1374	7	ACA34364		Aca34364	Prokaryot
26	812	35.9	110000	2	AAT42063_11		Continuation (12 o	
27	812	35.9	110000	2	AAT42063_12		Continuation (13 o	
28	795.5	35.2	2835	7	ACA27387		Aca27387	Prokaryot
29	783.5	34.6	1482	7	ACA39003		Aca39003	Prokaryot
30	783.5	34.6	100848	4	AAF28552		Aaf28552	Genomic f
31	777.5	34.4	1383	7	ACA42841		Aca42841	Prokaryot
c 32	775.5	34.3	69936	3	AAA81479		Aaa81479	N. mening
33	775.5	34.3	110000	3	AAA81490_04		Continuation (5 of	
34	775.5	34.3	349980	3	AAF21607		Aaf21607	Neisseria
35	772.5	34.2	1368	3	AAZ53149		Aaz53149	Neisseria
36	760	33.6	1359	3	AAZ53148		Aaz53148	Neisseria
37	757	33.5	1359	3	AAZ53150		Aaz53150	Neisseria
38	757	33.5	1359	7	ACA42011		Aca42011	Prokaryot
39	756	33.4	1364	7	ACA49178		Aca49178	Prokaryot
40	744	32.9	1308	7	ABZ41552		Abz41552	N. gonorr
41	744	32.9	1308	7	ACA41078		Aca41078	Prokaryot
42	731	32.3	1119	6	ABQ90030		Abq90030	M. capsul
43	729.5	32.3	1452	8	ADA30607		Ada30607	DNA encod
44	726.5	32.1	1398	7	ACA20661		Aca20661	Prokaryot
45	695	30.7	1158	7	ACA23517		Aca23517	Prokaryot

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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 24, 2004, 08:13:16 ; Search time 111 Seconds
(without alignments)
2289.797 Million cell updates/sec

Title: US-10-070-778-2
Perfect score: 2262
Sequence: 1 MLEPLRLSQLTVALDARLIG.....RSAAMDKVVAALCGSSEESH 458

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10070778/runat_23032004_141617_6682/app_query.fasta_1.
647

-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10070778 @CGN_1_1_85 @runat_23032004_141617_6682 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				DB	ID	Description
No.	Score	Match	Length	%				
c	1	2250	99.5	1515	4	US-09-252-991A-7701		Sequence 7701, Ap
	2	1691	74.8	1215	4	US-09-252-991A-7862		Sequence 7862, Ap
	3	885.5	39.1	1360	2	US-08-732-612-1		Sequence 1, Appli
	4	876.5	38.7	1437	4	US-09-489-039A-5205		Sequence 5205, Ap
	5	821.5	36.3	1419	4	US-09-543-681A-2913		Sequence 2913, Ap
	6	812	35.9	1830121	4	US-09-557-884-1		Sequence 1, Appli
	7	812	35.9	1830121	4	US-09-643-990A-1		Sequence 1, Appli
	8	784.5	34.7	1506	4	US-09-540-236-1209		Sequence 1209, Ap
	9	783.5	34.6	100848	4	US-09-596-002-39		Sequence 39, Appl
	10	729.5	32.3	1452	4	US-09-328-352-1894		Sequence 1894, Ap
c	11	687	30.4	640681	4	US-09-790-988-1		Sequence 1, Appli
	12	593	26.2	6911	1	US-08-311-174-4		Sequence 4, Appli
c	13	574	25.4	4411529	3	US-09-103-840A-1		Sequence 1, Appli
c	14	572	25.3	4403765	3	US-09-103-840A-2		Sequence 2, Appli
	15	551.5	24.4	7363	4	US-08-956-171E-19		Sequence 19, Appl
	16	544.5	24.1	1400	3	US-09-144-918-1		Sequence 1, Appli
	17	536.5	23.7	1374	4	US-09-134-001C-1447		Sequence 1447, Ap
	18	528	23.3	1404	4	US-09-252-991A-7623		Sequence 7623, Ap
	19	465.5	20.6	1452	4	US-09-134-000C-1457		Sequence 1457, Ap
	20	459.5	20.3	1847	4	US-08-961-527-196		Sequence 196, App
	21	452.5	20.0	1702	3	US-09-143-954-1		Sequence 1, Appli
	22	447.5	19.8	1676	3	US-09-143-954-3		Sequence 3, Appli
	23	420.5	18.6	1455	4	US-09-107-532A-356		Sequence 356, App
	24	416	18.4	1230025	4	US-09-198-452A-1		Sequence 1, Appli
c	25	276	12.2	1611	4	US-09-252-991A-7930		Sequence 7930, Ap
	26	273	12.1	1335	4	US-09-252-991A-7551		Sequence 7551, Ap
	27	271	12.0	1401	4	US-09-252-991A-7622		Sequence 7622, Ap
c	28	264.5	11.7	1230025	4	US-09-198-452A-1		Sequence 1, Appli
	29	263	11.6	1094	3	US-09-144-918-3		Sequence 3, Appli
	30	261.5	11.6	1509	4	US-09-489-039A-5144		Sequence 5144, Ap
	31	255	11.3	1509	4	US-09-543-681A-2855		Sequence 2855, Ap
	32	246	10.9	5757	3	US-08-984-618-1		Sequence 1, Appli
	33	245	10.8	1416	4	US-09-328-352-1282		Sequence 1282, Ap
	34	241	10.7	1542	4	US-09-252-991A-7625		Sequence 7625, Ap
c	35	241	10.7	1701	4	US-09-252-991A-7927		Sequence 7927, Ap
	36	232	10.3	1371	4	US-09-252-991A-7702		Sequence 7702, Ap
c	37	232	10.3	1401	4	US-09-252-991A-7861		Sequence 7861, Ap
	38	231	10.2	2600	3	US-08-988-251-1		Sequence 1, Appli
	39	231	10.2	2600	3	US-09-386-048-1		Sequence 1, Appli
	40	231	10.2	12658	4	US-08-956-171E-127		Sequence 127, App
	41	227.5	10.1	1503	4	US-09-328-352-2140		Sequence 2140, Ap
	42	224	9.9	1503	4	US-09-134-001C-1153		Sequence 1153, Ap
	43	220	9.7	1572	4	US-09-540-236-1219		Sequence 1219, Ap
	44	212	9.4	2193	2	US-08-934-481-1		Sequence 1, Appli
	45	212	9.4	2193	4	US-09-290-602-1		Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-252-991A-7701

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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 24, 2004, 09:10:24 ; Search time 2940 Seconds
(without alignments)
576.263 Million cell updates/sec

Title: US-10-070-778-2
Perfect score: 2262
Sequence: 1 MLEPLRLSQLTVALDARLIG.....RSAAMDKVVAALCGSSEESH 458

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2438257 seqs, 1849576744 residues

Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp

Q=/cgn2_1/USPTO_spool_p/US10070778/runat_23032004_141619_6746/app_query.fasta_1.
647

-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10070778 @CGN_1_1_333 @runat_23032004_141619_6746
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2258	99.8	1377	9	US-09-815-242-7914	Sequence 7914, Ap
2	2258	99.8	1377	12	US-10-282-122A-30470	Sequence 30470, A
3	1616	71.4	1356	12	US-10-282-122A-33530	Sequence 33530, A
4	1603.5	70.9	1365	12	US-10-282-122A-32131	Sequence 32131, A
5	917.5	40.6	1359	9	US-09-741-669-257	Sequence 257, App
6	917.5	40.6	1359	9	US-09-815-242-5930	Sequence 5930, Ap
7	917.5	40.6	1359	12	US-10-282-122A-20227	Sequence 20227, A
8	882.5	39.0	1356	12	US-10-282-122A-19658	Sequence 19658, A
9	880.5	38.9	1359	12	US-10-282-122A-38999	Sequence 38999, A
10	879.5	38.9	1356	12	US-10-282-122A-23403	Sequence 23403, A
11	875.5	38.7	1362	12	US-10-282-122A-41276	Sequence 41276, A
12	874	38.6	1404	12	US-10-282-122A-14163	Sequence 14163, A
13	871.5	38.5	1359	12	US-10-282-122A-39833	Sequence 39833, A
14	870.5	38.5	1359	9	US-09-815-242-9976	Sequence 9976, Ap
15	857	37.9	1377	12	US-10-282-122A-41735	Sequence 41735, A
16	828	36.6	1410	12	US-10-282-122A-12920	Sequence 12920, A
17	819	36.2	1380	12	US-10-282-122A-32631	Sequence 32631, A
18	812	35.9	1374	9	US-09-815-242-7088	Sequence 7088, Ap
19	812	35.9	1374	12	US-10-282-122A-22234	Sequence 22234, A
20	812	35.9	1830121	14	US-10-329-960-1	Sequence 1, Appli
21	812	35.9	1830121	15	US-10-329-670-1	Sequence 1, Appli
22	795.5	35.2	2835	12	US-10-282-122A-15257	Sequence 15257, A
23	783.5	34.6	1482	12	US-10-282-122A-26873	Sequence 26873, A
24	777.5	34.4	1383	12	US-10-282-122A-30711	Sequence 30711, A
25	757	33.5	1359	12	US-10-282-122A-29881	Sequence 29881, A
26	756	33.4	1364	12	US-10-282-122A-37048	Sequence 37048, A
27	744	32.9	1308	12	US-10-282-122A-28948	Sequence 28948, A
28	726.5	32.1	1398	12	US-10-282-122A-8531	Sequence 8531, Ap
29	702.5	31.1	9025608	14	US-10-156-761-1	Sequence 1, Appli
30	701.5	31.0	1413	14	US-10-156-761-6095	Sequence 6095, Ap
31	695	30.7	1158	12	US-10-282-122A-11387	Sequence 11387, A
c 32	687	30.4	640681	9	US-09-790-988-1	Sequence 1, Appli
33	618	27.3	1542	9	US-09-738-626-2369	Sequence 2369, Ap
c 34	618	27.3	3309400	9	US-09-738-626-1	Sequence 1, Appli
35	604.5	26.7	1488	12	US-10-282-122A-17843	Sequence 17843, A
36	572.5	25.3	1374	12	US-10-282-122A-9891	Sequence 9891, Ap
37	569	25.2	1533	9	US-09-712-363-81	Sequence 81, Appl
38	569	25.2	1533	12	US-10-282-122A-28471	Sequence 28471, A
39	556.5	24.6	1353	9	US-09-815-242-4300	Sequence 4300, Ap